

<https://helda.helsinki.fi>

Towards a coordinated strategy for intercepting human disease emergence in Africa

Forbes, Kristian M.

2021-02

Forbes , K M , Anzala , O , Carlson , C J , Kelvin , A A , Kuppalli , K , Leroy , E M , Maganga , G D , Masika , M M , Mombo , I M , Mwaengo , D M , Niama , R F , Nziza , J , Ogola , J , Pickering , B S , Rasmussen , A L , Sironen , T , Vapalahti , O , Webala , P W & Kindrachuk , J 2021 , ' Towards a coordinated strategy for intercepting human disease emergence in Africa ' , The Lancet microbiome , vol. 2 , no. 2 , pp. E51-E52 . [https://doi.org/10.1016/S2666-5247\(20\)30220-2](https://doi.org/10.1016/S2666-5247(20)30220-2)

<http://hdl.handle.net/10138/328639>

[https://doi.org/10.1016/S2666-5247\(20\)30220-2](https://doi.org/10.1016/S2666-5247(20)30220-2)

cc_by

publishedVersion

Downloaded from Helda, University of Helsinki institutional repository.

This is an electronic reprint of the original article.

This reprint may differ from the original in pagination and typographic detail.

Please cite the original version.

Towards a coordinated strategy for intercepting human disease emergence in Africa



Emerging zoonotic viruses are one of the greatest threats to human health and security, as evidenced by the increasing frequency of disease outbreaks.¹ To date, the main pre-emptive response to these outbreaks has been extensive, cost-heavy efforts to document virus diversity in wildlife (eg, PREDICT and the Global Virome Projects).^{2,3} Although these efforts have resulted in the identification of thousands of novel viruses, fewer than 1% are described to date, substantial challenges remain around access and benefit sharing from viral discovery programmes, and—perhaps most problematic for public health application—the spillover hazard of these viruses can only be coarsely inferred at present.^{4–6}

Our ability to control and restrict the spread of infectious diseases is critically dependent on early detection. This vigilance should include viruses that might not pose immediate or widespread public health threats, but where repeated spillover or persistent, unchecked transmission chains in humans provides latitude for the evolution of increased pathogenicity, host immune evasion mechanisms, and efficient human-to-human transmission.⁷ Building on existing research, here we emphasise the importance of a coordinated and targeted strategy for early detection of virus spillover and emergence in humans. This model is based on inter-related study or evidence types and is a collaborative framework geared towards African and other low-income and middle-income countries where risk of disease emergence is often great, infectious disease-related morbidity and mortality are over-represented compared with in high-income regions, undescribed virus diversity is high, and resources are constrained.

For this strategy we highlight four complementary study or evidence types indicative of past or current unknown infection: procurement and screening of diagnostic samples from undiagnosed patients, analysis of samples from suspicious fatalities of unknown cause, serosurveys of high-risk or sentinel groups, and analysis of archived samples (appendix p 1). Approaches might overlap (eg, death and post-mortem analysis of undiagnosed patients) but are independently capable of detecting separate evidence for pathogen

spillover and novel disease emergence. Their concurrent implementation heightens detectability.

Collecting and screening samples from patients with undiagnosed febrile illness provides an efficient means to target the subset of populations most likely to have novel infectious diseases. With properly trained staff and systems, sample collections can be implemented at the point of care for continuous monitoring. When possible, collecting and screening samples from people with an unknown cause of death can identify cases of severe disease that might not remain in hospitals sufficiently long for inclusion in a monitoring strategy, present with unusual symptoms, or develop severe disease but not present to a hospital or clinic, as is likely to occur in low-income and middle-income countries where traditional medicine is practiced. Although new technologies such as next-generation sequencing are increasingly available for detection of unknown viruses, linking clinical findings to disease aetiology can be a challenge. Due consideration must also be given to sample types for collection and their appropriate storage.

By contrast, serosurveys or screening of sentinel groups are proactive studies implemented by researchers to collect blood samples from individuals at greatest risk of exposure to zoonotic viruses. Such individuals include pastoralists, agriculture workers, game hunters, traders, or others working in close contact with wildlife. Studies can detect antibodies indicative of spillover events, including asymptomatic cases, and use increasingly efficient and cost-effective screening methods. Likewise, archived samples provide varied, potentially copious, and readily available sample sources that are appropriate for detection of viruses and antibodies indicative of spillover across longer timescales. Like focused serosurveys, archived samples can be especially powerful for identifying viruses that are silently circulating among humans or rare spillover events that could have future implications. These samples also provide important datapoints for efforts to track the effect of global environmental changes on virus spillover, given that most forecasting efforts do not have empirical real-time validation. An important limitation of antibody surveillance is the inability to

Published Online
December 17, 2020
[https://doi.org/10.1016/S2666-5247\(20\)30220-2](https://doi.org/10.1016/S2666-5247(20)30220-2)

See Online for appendix

identify active infections or specific viruses. But these approaches can prompt and guide focused investigation and are integral to a comprehensive strategy.

None of the methods or evidence types that we describe here are novel tools and each has limitations;^{8–10} however, we highlight the value of a cohesive, targeted, and widespread approach for maximising the likelihood of detecting novel infections (appendix p 1). We acknowledge that in some settings or situations some of the proposed approaches might not be appropriate or might need to be adapted.

Ongoing research aims to develop predictive tools so that we might be able to infer the zoonotic potential of the ever-increasing number of newly identified wildlife viruses from their genetic sequence. Meanwhile, comprehensive systems for early detection and containment of wildlife virus spillover and emergence remain one of our strongest responses against the threat posed by zoonotic viruses.

We declare no competing interests. We are members of the new Consortium for Intercepting Emerging Diseases in Africa. KMF is supported by grants from the National Science Foundation (NSF; grant number DEB 1911925) and the Arkansas Biosciences Institute. JK is supported by a Tier 2 Canada Research Chair in the Molecular Pathogenesis of Emerging and Re-Emerging Viruses provided by the Canadian Institutes of Health Research (grant number 950-231498). CJC is supported by NSF (grant number BII 2021909) through the Verena Consortium, and thanks the consortium for formative discussions.

Copyright © 2020 The Author(s). Published by Elsevier Ltd. This is an Open Access article under the CC BY 4.0 license.

***Kristian M Forbes, Omu Anzala, Colin J Carlson, Alyson A Kelvin, Krutika Kuppalli, Eric M Leroy, Gael D Maganga, Moses M Masika, Illich M Mombo, Dufton M Mwaengo, Roch F Niama, Julius Nziza, Joseph Ogola, Brad S Pickering, Angela L Rasmussen, Tarja Sironen, Olli Vapalahti, Paul W Webala, Jason Kindrachuk**
kmforbes@uark.edu

Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701, USA (KMF); KAVI Institute of Clinical Research (OA, MMM, JO), Institute of Tropical and Infectious Diseases (DMM), University of Nairobi, Nairobi, Kenya; Center for Global Health Science and Security, Georgetown University Medical Center, Washington, DC, USA (CJC, ALR); Vaccine and Infectious Disease Organization-International Vaccine Centre, University of Saskatchewan, Saskatoon, SK, Canada (AAK, JK); Department of Pediatrics, Dalhousie University, and Canadian Centre for Vaccinology, IWK Health Centre, Halifax, NS, Canada (AAK); Division of Infectious Diseases, Medical University of South Carolina, Charleston, SC, USA (KK); French National Research Institute for Sustainable Development, Infectious Diseases and Vectors: Ecology, Genetics, Evolution and Control Unit, Montpellier, France (EML); Department of Virology, Interdisciplinary Centre of Medical Research of Franceville, and Institut National Supérieur d'Agronomie et de Biotechnologies, Université des Sciences et Techniques de Masuku, Franceville, Gabon (GDM); Department of Virology, Interdisciplinary Centre of Medical Research of Franceville, Franceville, Gabon (IMM); Marien Ngouabi University, Brazzaville, Republic of the Congo (RFN); Gorilla Doctors, Musanze, Rwanda (JN); National Centre for Foreign Animal Disease, Canadian Food Inspection Agency (BSP), Department of Medical Microbiology and Infectious Diseases (BSP, JK), University of Manitoba, Winnipeg, MB, Canada (BSP); Department of Veterinary Microbiology and Preventive Medicine, Iowa State University, Ames, IA, USA (BSP); Helsinki One Health (TS), Department of Virology and Department of Veterinary Biosciences (OV), University of Helsinki, Helsinki, Finland; HUSLAB, Helsinki University Hospital, Helsinki, Finland (TS, OV); Maasai Mara University, Narok, Kenya (PWW)

- 1 Morens DM, Fauci AS. Emerging pandemic diseases: how we got to COVID-19. *Cell* 2020; **182**: 1077–92.
- 2 Morse SS, Mazet JAK, Woolhouse M, et al. Prediction and prevention of the next pandemic zoonosis. *Lancet* 2012; **380**: 1956–65.
- 3 Carroll D, Daszak P, Wolfe ND, et al. The Global Virome Project. *Science* 2018; **359**: 872–74.
- 4 Rourke M. Viruses for sale – all viruses are subject to access and benefit sharing obligations under the convention on biological diversity. Griffith University Law School Research Paper No. 17-14, June 17, 2017. https://papers.ssrn.com/sol3/papers.cfm?abstract_id=2984046 (accessed Nov 30, 2020).
- 5 Carlson CJ, Zipfel CM, Garnier R, Bansal S. Global estimates of mammalian viral diversity accounting for host sharing. *Nat Ecol Evol* 2019; **3**: 1070–75.
- 6 Carlson CJ. From PREDICT to prevention, one pandemic later. *Lancet Microbe* 2020; **1**: e6–7.
- 7 Holmes EC. On the origin and evolution of the human immunodeficiency virus (HIV). *Biol Rev Camb Philos Soc* 2001; **76**: 239–54.
- 8 Wolfe ND, Heneine W, Carr JK, et al. Emergence of unique primate T-lymphotropic viruses among central African bushmeat hunters. *Proc Natl Acad Sci USA* 2005; **102**: 7994–99.
- 9 Forbes KM, Webala PW, Jääskeläinen AJ, et al. Bombali virus in *Mops condylurus* bat, Kenya. *Emerg Infect Dis* 2019; **25**: 955–57.
- 10 Steffen I, Lu K, Hoff NA, et al. Seroreactivity against Marburg or related filoviruses in west and central Africa. *Emerg Microbes Infect* 2020; **9**: 124–28.

For the Verena consortium website see <https://www.viralemergence.org/>